

FIGURE 1

AFP E1a and E1b Adenovirus Constructs

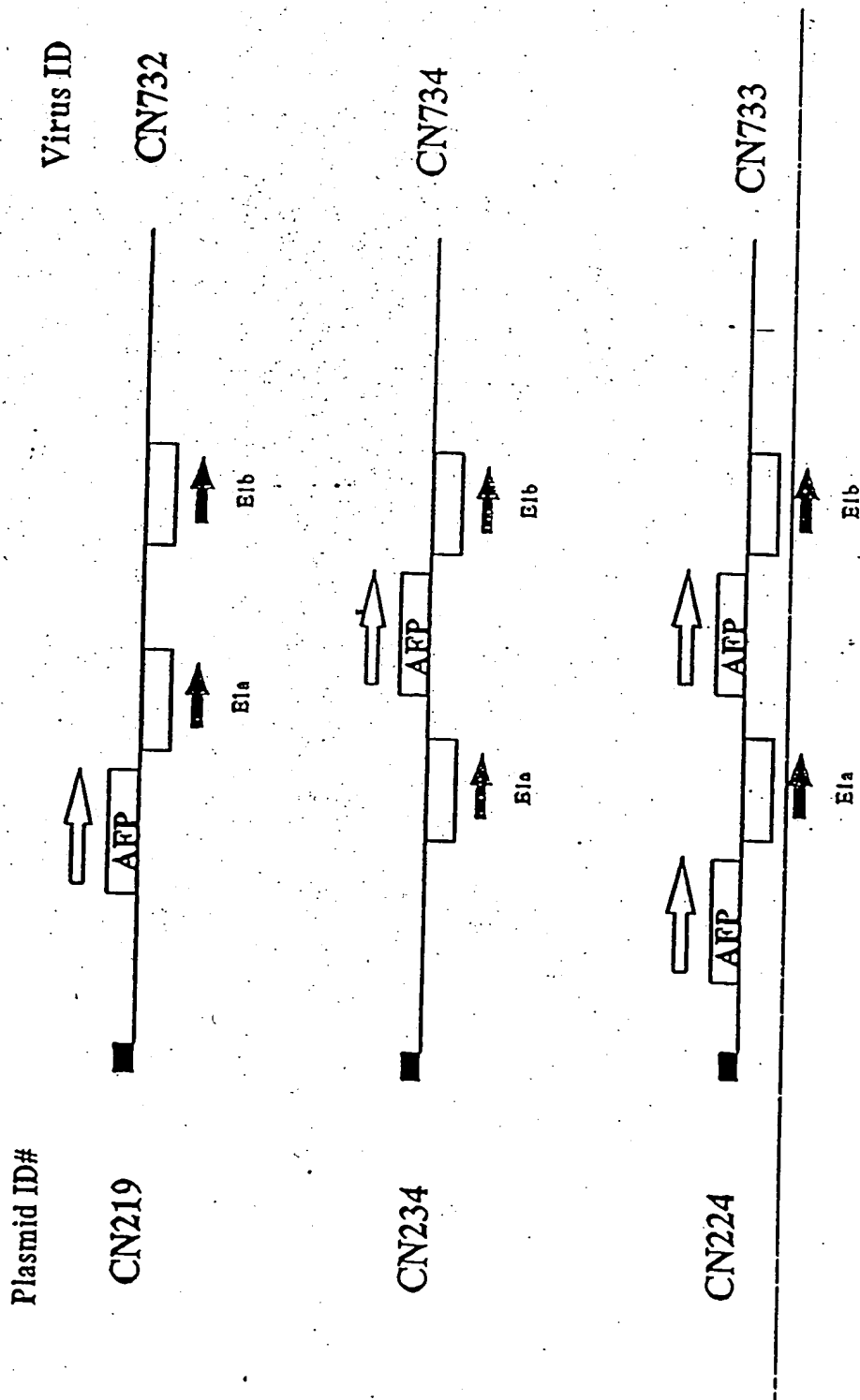


FIGURE 2A

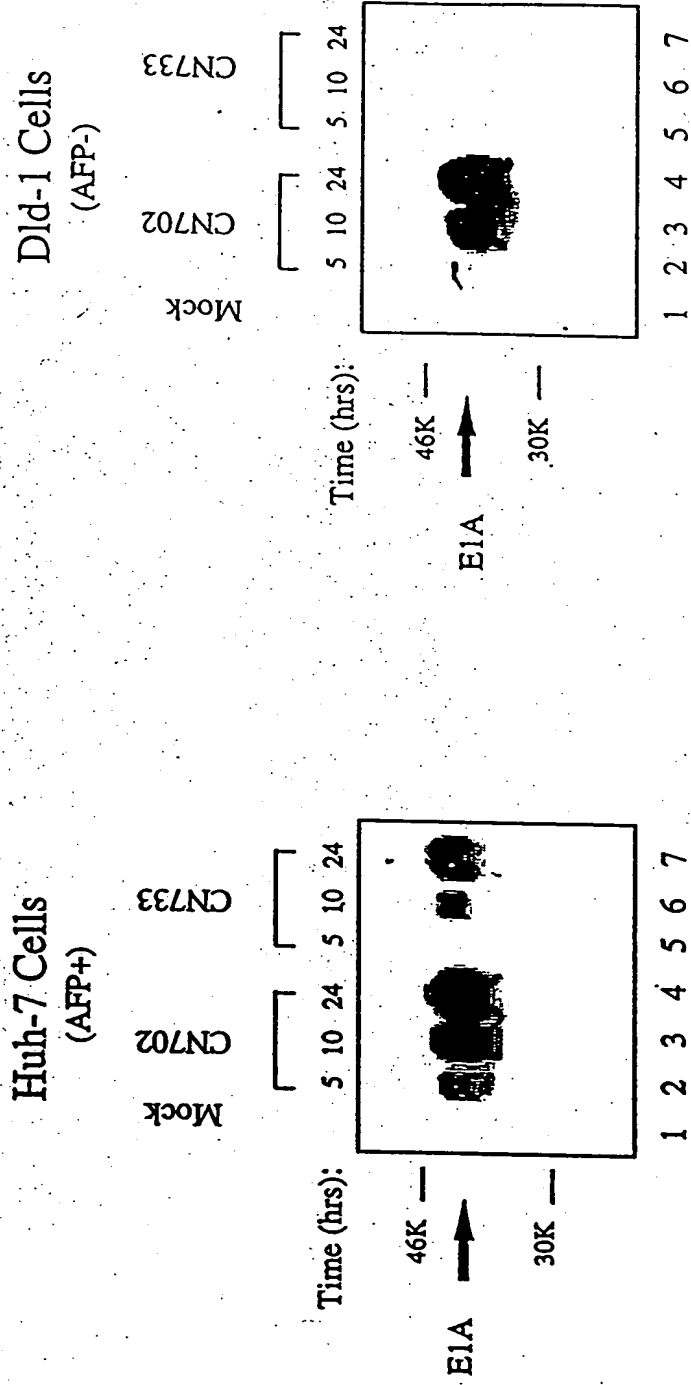


FIGURE 2B

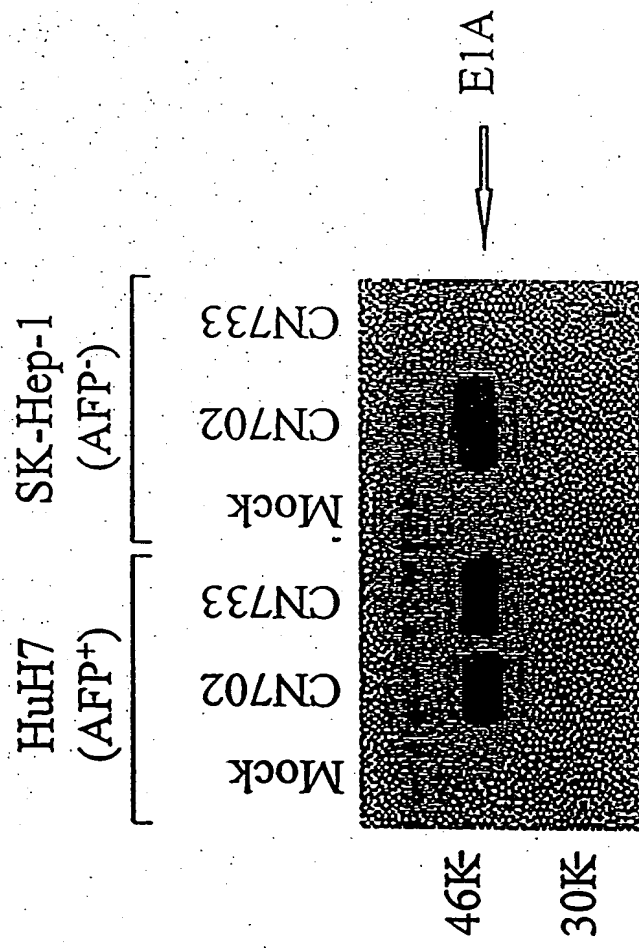


FIGURE 3A

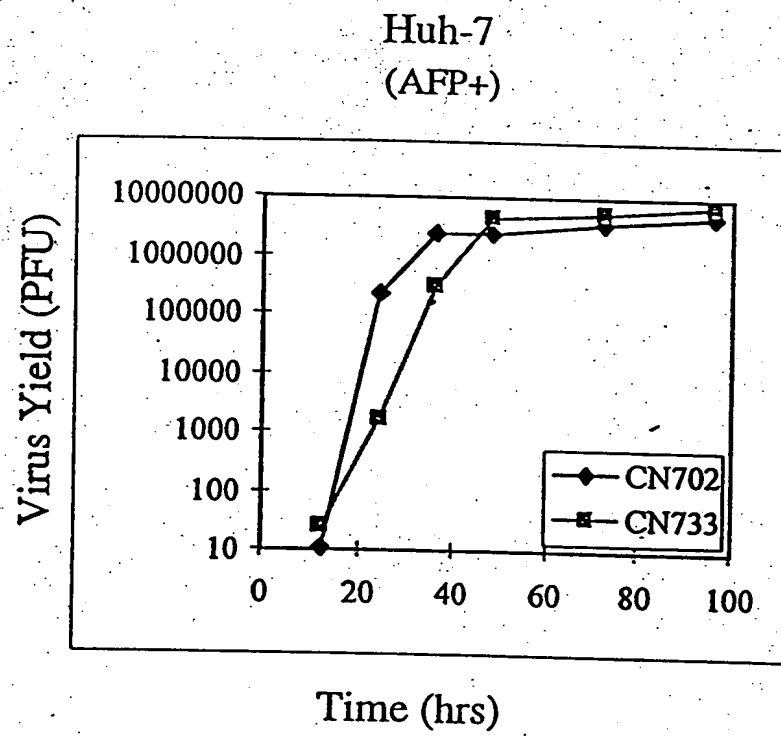


FIGURE 3B

Sk-Hep-1
(AFP-)

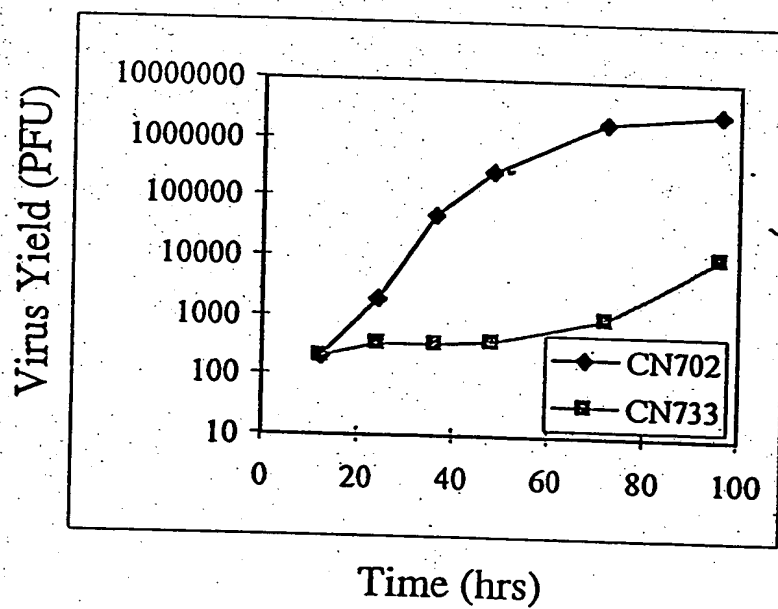


FIGURE 3C

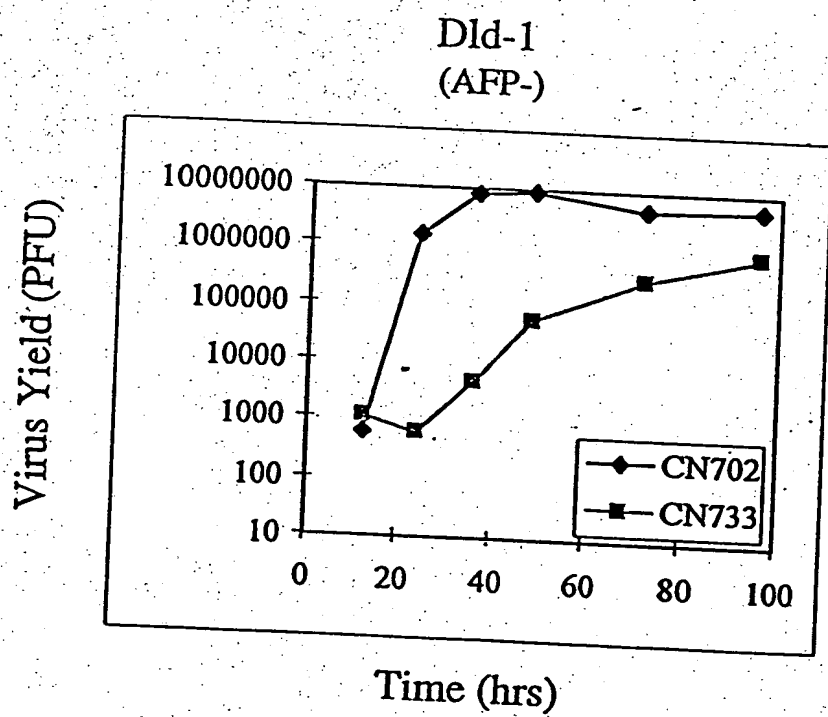


FIGURE 4A

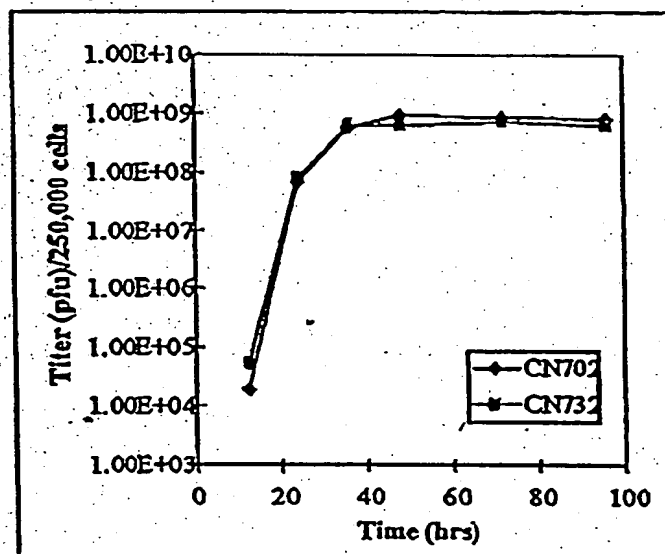


FIGURE 4B

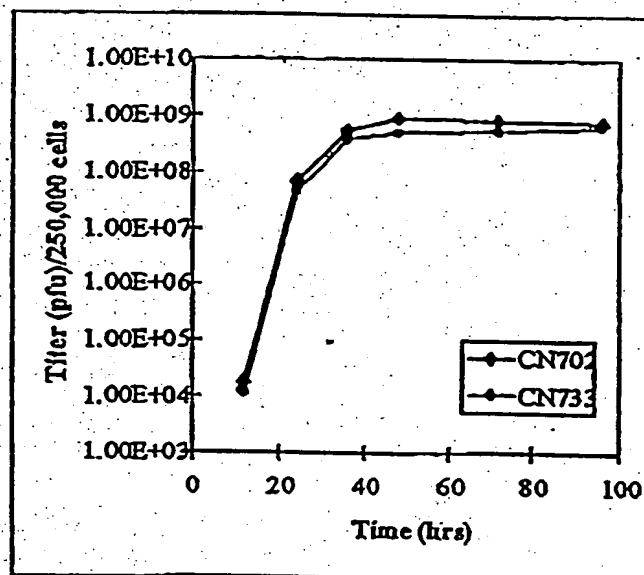


FIGURE 4C

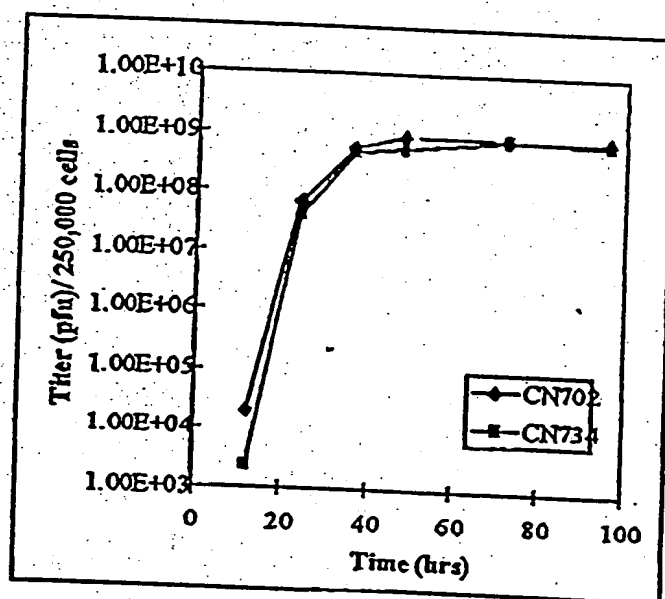


FIGURE 5A

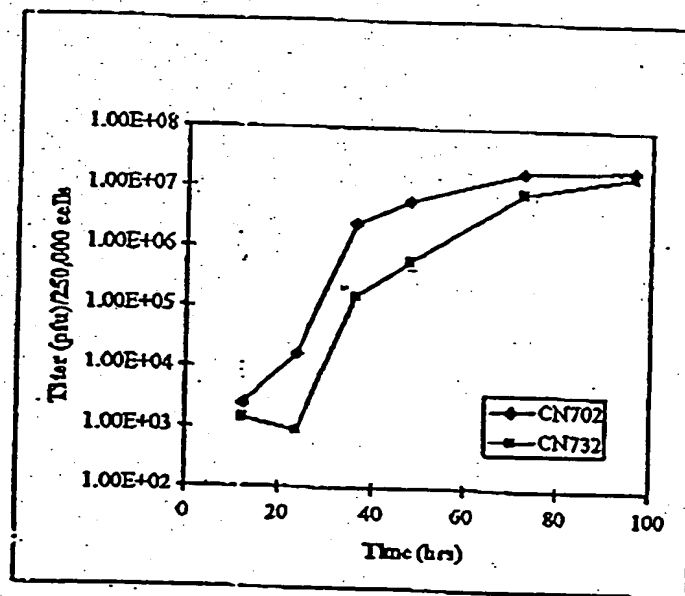


FIGURE 5B

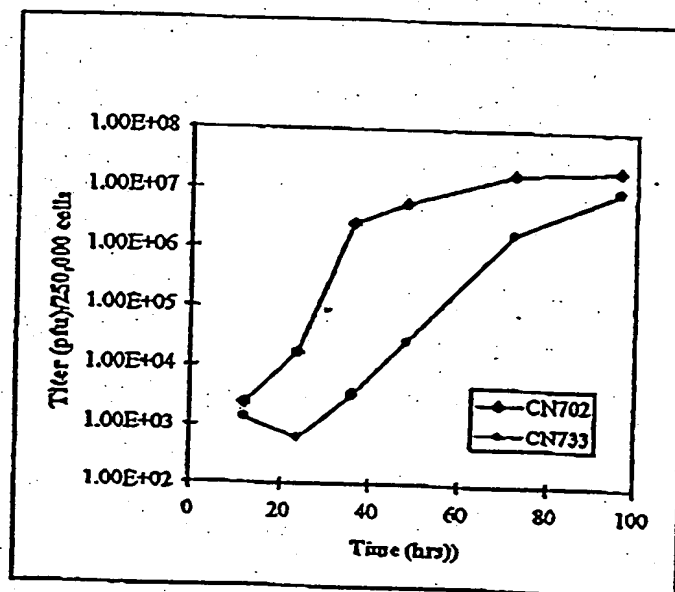


FIGURE 6A

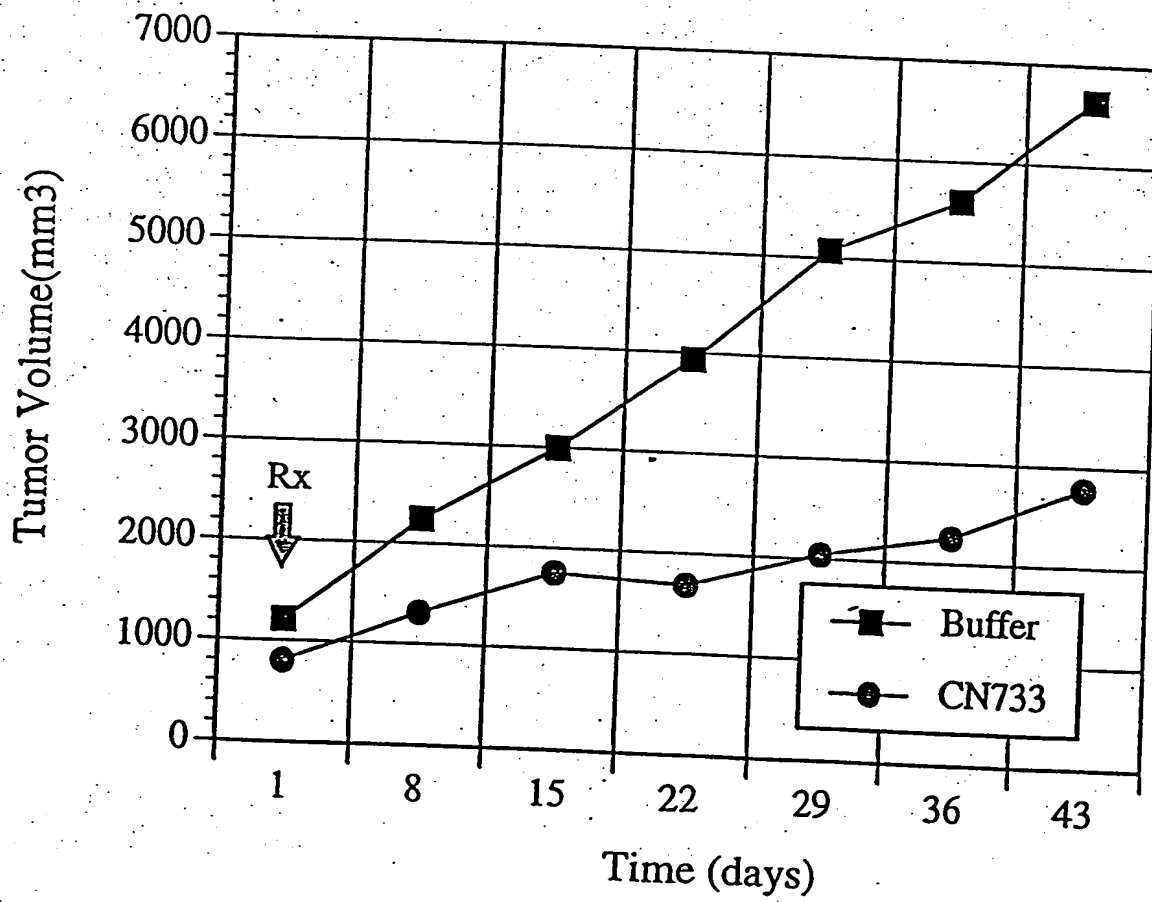
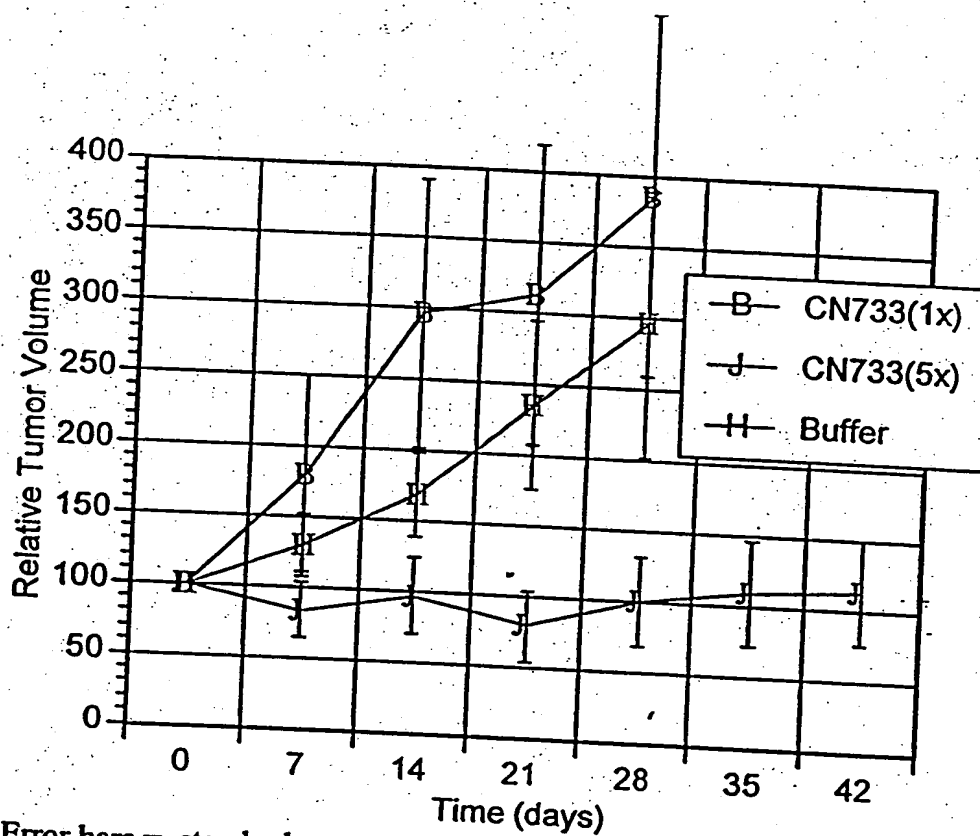


FIGURE 6B



Error bars = standard error

Animals from groups treated with a single dose of CN733 and buffer were sacrificed at 28 days because of excessive tumor burden

FIGURE 7

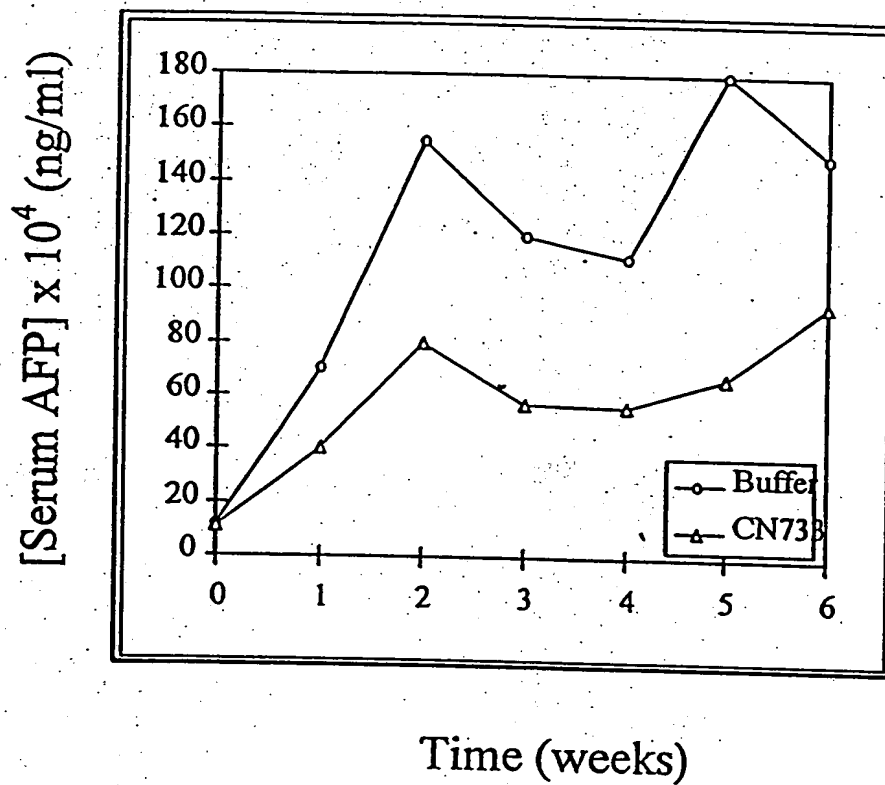
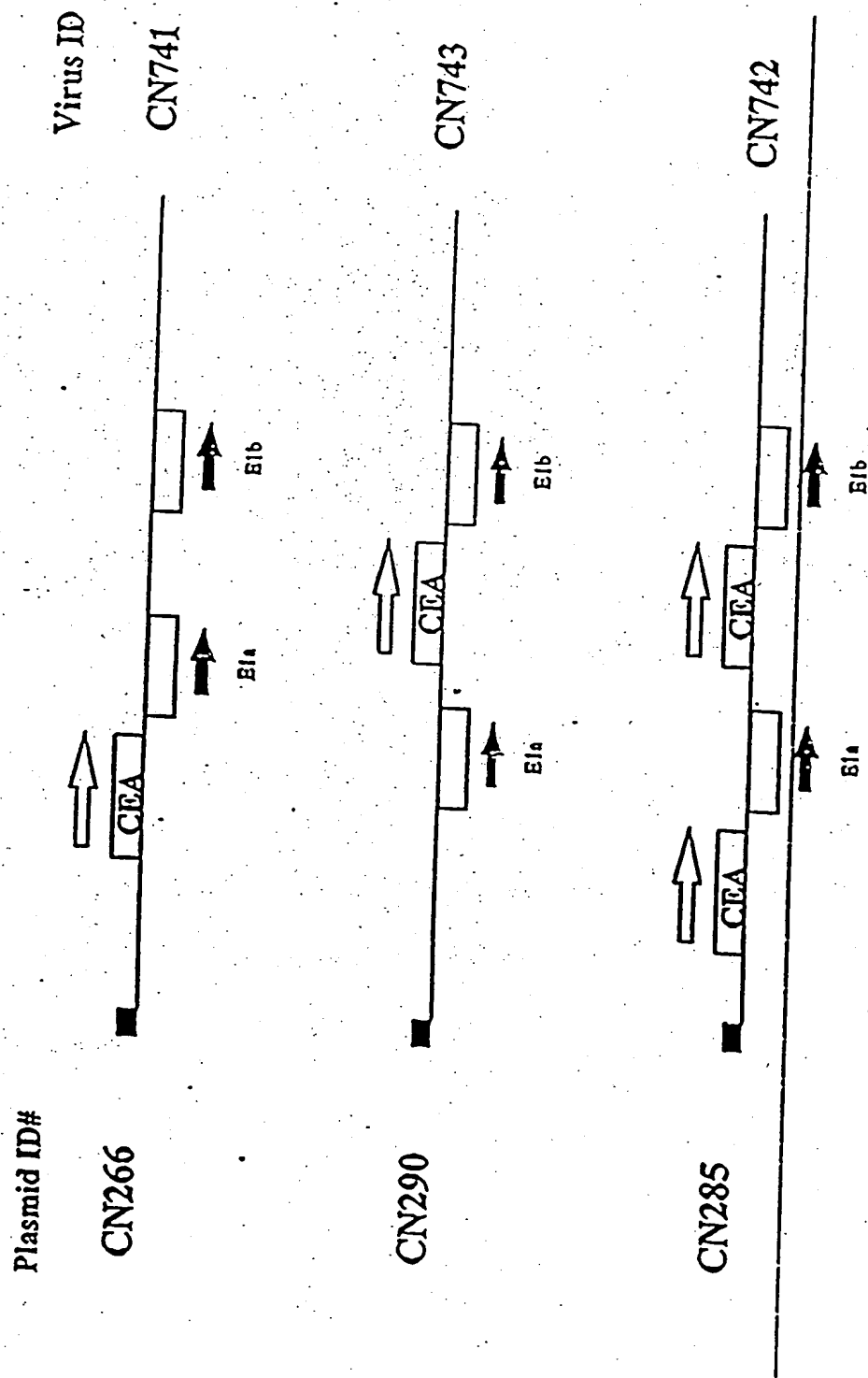


FIGURE 8

CEA E1a and E1b Adenovirus Constructs



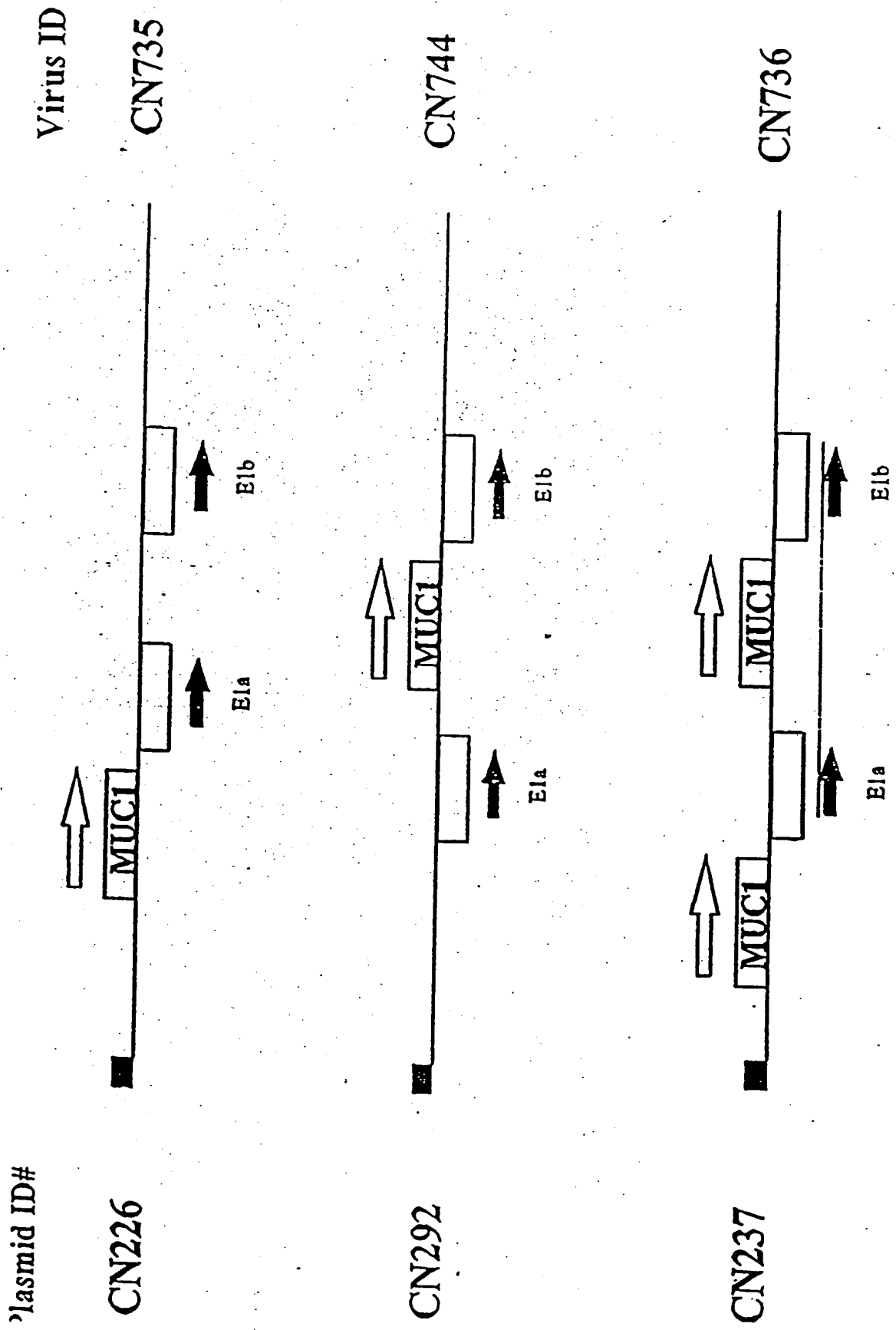


FIGURE 9

-426

5'-AAGCTTCCACAAGTGCATTTAGCCTCTCCAGTATTGCTGATGAATCCACAGT
TCAGGTTCAATGGCGTTCAAACTTGATGAAAAATGACCAGACTTTATATTCTTA
CACCAACATCTATCTGATTGGAGGAATGGATAATAGTCATCATGTTTAAACATCT
ACCATCCAGTTAAGAAAATATGATAGCACTTGTCTTACTCTTTTCTTAATA

ARE-1

GGGACATAAAGCCCACAAATAAAAAATATGCCTGAAGAATGGGACAGGCATTGG
GCATTGTCCATGCCTAGTAAAGTACTCCAAGAACCTATTGTATACTAGATGACA

ARE-2

CAATGTCAATGTCTGTGTACAACCTGCCAAGTGGGATGCAAGACACTGCCCATG

+1

CAATCATCCTGAAAAGCAGCTATAAAAAGCAGGAAGCTACTCTGCACCTT

CAAT box

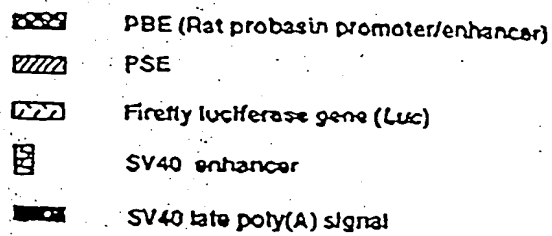
TATAA box

Transcription site

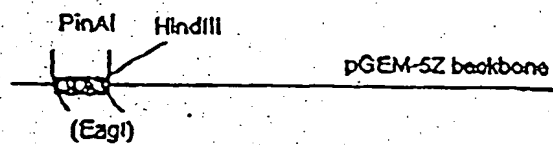
+28

GTCAGTGAGGTCCAGATACCTACAG-3'

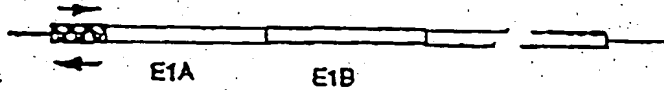
FIGURE 10



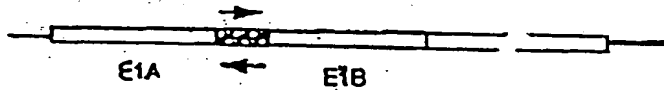
CN249
 (CN250)
 CN258
 CN271



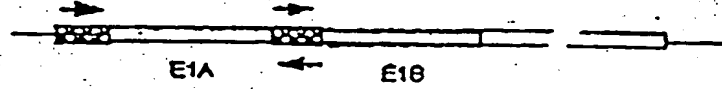
CN251
 CN253



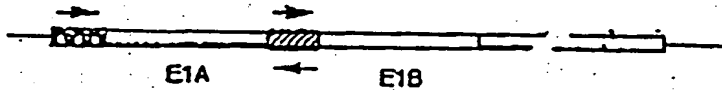
CN254 (CN275)
 CN255 (CN276)



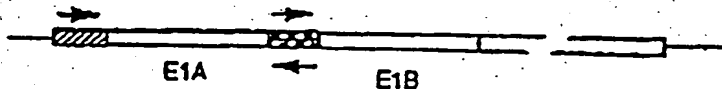
CN288
 CN269



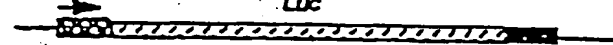
CN257
 CN258



CN273
 CN274



CN280



CN281

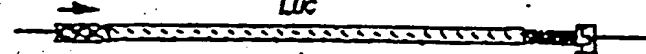


FIGURE 11

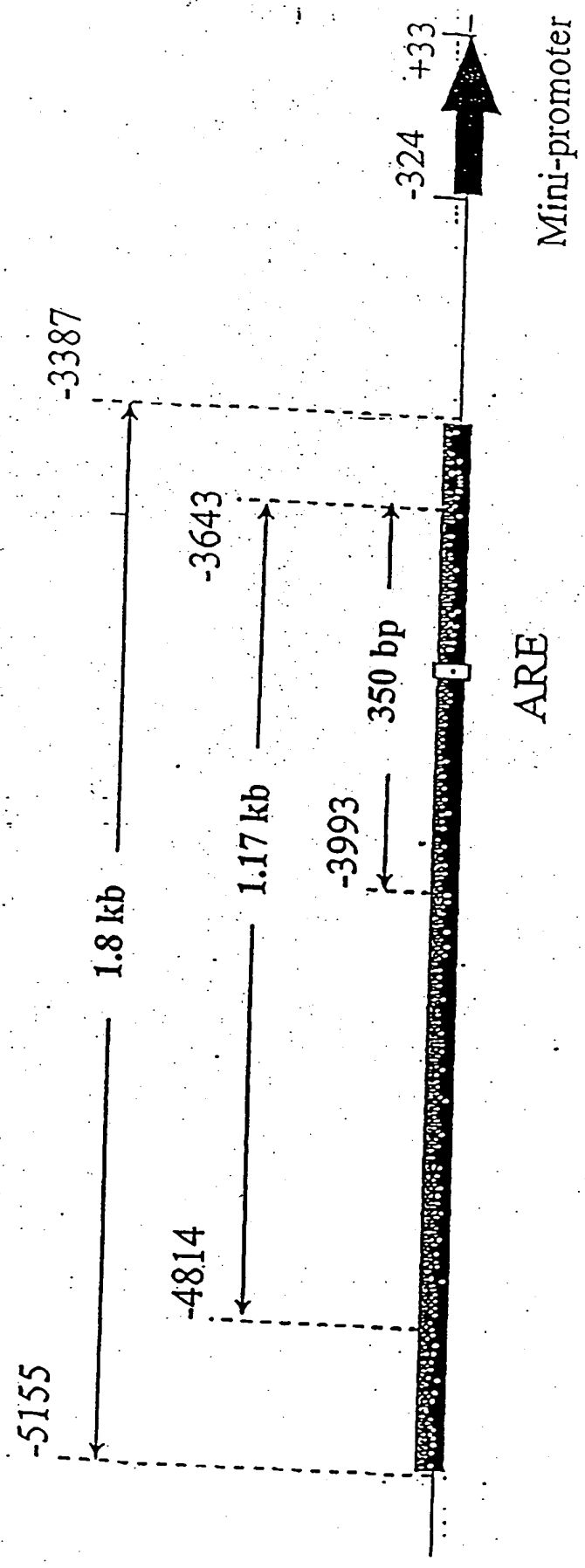


FIGURE 12

hKLK2 P

CN749



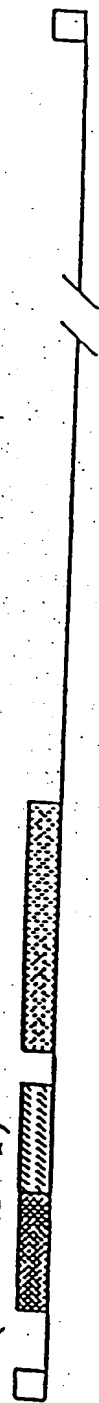
E1A E1B

CN702



hKLK2
(1.8 kb E + P)

CN763



hKLK2
(1.17 kb E + P)

CN768



FIGURE 13

FIGURE 14A

aagcttttta gtgctttaga cagtgaagctg gtctgtctaa cccaagtgaac ctgggctcca	60
tactcagccc cagaagtga gggatgaagct gggatggagcc aaaccaggca agcctaccct	120
cagggctccc agtggcctga gaaccattgg acccaggacc cattacttct agggtaagga	180
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tacctgggag aggagcaggc aaactatcac tgccccaggt tctctgaaca gaaacagagg	300
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gctcatgttc ccaatccagg agaatgcatt tgggatctgc cttcttctca ctccttggtt	480
agcaagacta agcaaccagg actctggatt tggggaaaga cgtttatttg tggaggccag	540
tgatgacaat cccacgaggg cctaggtgaa gagggcagga aggctcgaga cactggggac	600
tgagtgaata ccacacccat gatctgcacc acccatggat gctccttcat tgcctacctt	660
tctgttgata tcagatggcc ccattttctg taccttcaca gaaggacaca ggctagggtc	720
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ctcctgggtc ctgcagggcc agaacattca tcaccatac tgacctcta gatgggaatg	840
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gaggaagggc catcgagacc cagcctggaa ggttcttgct tctgaccatc caggatttac	960
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ctgataaccc aggaccatt acttctaggg taaggagggt ccaggagaca gaagctgagg	1140
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gactctctac tcaggcctg acatgctgaa ataggacaat ggccttgctc tctctcccca	1440
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ccagcctgtc caggcccttc cactctccac tttgtgacca tgtccaggac caccctcag	1620
atcctgagcc tgcaaatacc cccttgctg gtgggtggat tcagtaaaca gtgagctct	1680

FIGURE 14B

atccagcccc cagagccacc tctgtcacct tctgtctggg catcatccca ccttcacaag	1740
cactaaagag catggggaga cctggctagc tgggtttctg catcacaag aaaataatcc	1800
cccaggttcg gattcccagg gctctgtatg tggagctgac agacctgagg ccaggagata	1860
gcagaggtca gccctagggg ggggtgggtca tccaccagg ggacaggggt gcaccagcct	1920
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cagcagtcag aggaggccat ggcagtggct gagtcctgc tccaggcccc aacagaccag	2040
accaacagca caatgcagtc cttccccaac gtcacaggtc accaaaggga aactgagggtg	2100
ctacctaac ttagagccat caggggagat aacagcccaa tttcccaaac aggccagttt	2160
caatcccatg acaatgacct ctctgtcttc attcttccca aaataggacg ctgattctcc	2220
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cagccctggc ctgggcctgt cccctgagag gtgttgggag aagctgagtc tctggggaca	3300
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FIGURE 14C

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tgactttctgc gtctgtccca gtcaccctga aaccacaaca aaaccccagc cccagaccct	3480
gcaggtacaa tacatgtggg gacagtctgt acccagggga agccagttct ctcttcctag	3540
gagaccgggc ctcagggtg tgcccggggc aggcgggggc agcacgtgcc tgtccttgag	3600
aactcgggac cttaagggc tctgctctgt gaggcacagc aaggatcctt ctgtccagag	3660
atgaaagcag ctctgcccc tctctgacc tcttctctt tcccaaattt caaccaacaa	3720
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caatggattg acaacatcaa gagttggaac aagtggacat ggagatgtta cttgtggaaa	3840
tttagatgtg ttcagctatc gggcaggaga atctgtgtca aattccagca tggttcagaa	3900
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agacgccaat gacaataaaa agagggacct ccgtcaccgc gtaaacatgt ccacacagct	5100

FIGURE 14D

ccagcaagca cccgtcttcc cagtgaatca ctgtaacctc ccctttaatc agccccaggc	5160
aaggctgcct gcgatggcca cacaggctcc aaccctgtgg cctcaacctc ccgcagaggc	5220
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acaaacacac acacacacac acacacacac acacacacac acagggaaag tgcaggatcc	5940
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agggagctgg gtactgccct ccagggaggc aggagcactg ttcccaacag agagcacatc	6300
ttcctgcagc agctgcacag acacaggagc ccccatgact gccctgggcc aggggtgtga	6360
ttccaaattt cgtgccccat tgggtgggac ggaggttgac cgtgacatcc aaggggcatc	6420
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taggggtgtc aagagagctg ggcattccac agagctgcac aagatgacgc ggacagaggg	6780

FIGURE 14E

tgacacaggg	ctcagggctt	cagacgggtc	gggaggctca	gctgagagtt	cagggacaga	6840
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aagcctgagt	gctctaagga	aatgctccca	ccccgatgta	gcctgcagca	ctggacggtc	6960
tgtgtacctc	cccgtgccc	atcctctcac	agcccccgcc	tctagggaca	caactcctgc	7020
cctaacatgc	atctttcctg	tctcattcca	cacaaaaggg	cctctgggggt	ccctgttctg	7080
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FIGURE 14F

gaaaacatgt tttattaaga ggaaaaatct aggctagaag tgctttatgc tcttttttct	8580
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gtaaatgtta tcaactgactg gatagtgttg gtgtctcact cccaaccct gtgtggtgac	8700
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FIGURE 14G

acaccagtgt ctaagcccct gatgagaaca ggggtggtctc tcccatatgc ccataccagg	10260
cctgtgaaca gaatcctcct tctgcagtga caatgtctga gaggacgaca tgtttcccag	10320
cctaacgtgc agccatgccc atctacccac tgcctactgc aggacagcac caaccagga	10380
gctgggaagc tgggagaaga catggaatac ccatggcttc tcaccttctt ccagtcaggt	10440
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cctaggtgcc tctgggaggc cgaggcagga gaattgcttg aaccggggag gcagaggttg	10560
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agaggaggac acaggctctg tggggctgca gcccaggatg ggactaagtg tgaagacatc	11760
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FIGURE 14H

tcctcatgcc cctctctctc aaatatgatt tggatctatg tccccgccca aatctcatgt	12000
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FIGURE 14I

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FIGURE 15A

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FIGURE 15B

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FIGURE 15C

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FIGURE 15D

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FIGURE 16A

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 aaaataggac gaaggtgaaa tattaggtag gaaaagtata atagttgaaa gaagtaaaaa 1260
 aaaatatgca tgagtagcag aatgtaaaag aggtgaagaa cgtaatatgtg actttttaga 1320
 ccagattgaa ggacagagac agaaaaattt taaggaattg ctaaaccatg tgagtgttag 1380
 aagtacagtc aataacatta aagcctcagg aggagaaaag aataggaaaag gaggaaatat 1440
 gtgaataaat agtagagaca tgtttgatgg attttaaaat atttgaaaga cctcacatca 1500
 aaggattcat accgtgccat tgaagaggaa gatggaaaag ccaagaagcc agatgaaagt 1560
 tagaaatatt attggcaaag cttaaattgtt aaaagtccta gagagaaaagg atggcagaaa 1620
 tattggcggg aaagaatgca gaacctagaa tataaattca tcccacagt ttggtagtgt 1680

FIGURE 16B

gcagctgtag ccttttctag ataatacact attgtcatac atcgcttaag cgagtgtaaa 1740
atggtctcct cactttatctt atttatatat ttatttagtt ttgagatgga gcctcgctct 1800
gtctcctagg ctggagtga atagtggat accactcact gcaacctctg cctcctctgt 1860
tcaagtgatt ttcttacctc agcctcccga gtagctggga ttacaggtgc gtgccaccac 1920
acccggctaa tttttgtatt tttttagag acggggtttt gccatgttg ccaggctgg 1980
cttgaactcc tgacatcagg tgatccacct gccttggcct cctaaagtgc tgggattaca 2040
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FIGURE 16C

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tctgatgac agtgacgatg agcatttttt catatttggt ggctgcttgt acgtcttttg 3480
agaagtgtct cttcatgcct tttggccact ttaatgggat tattttttgc tttttagttt 3540
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tcttccattc tgtaggttgt ctgtttactc tattgatggc ttcttttgct gtgccgaagc 3660
atcttiagttt aattagaaac cacctgccaa tttttgtttt tgttgcaatt gcttttgggg 3720
acttagtcat aaactctttg ccaaggtctg ggtcaagaag agtatttctt aggttttctt 3780
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ttgtatatgt gaaaggtcta ctctcatttt ctttccctct ttctttcttt ctttcttttc 3900
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FIGURE 16D

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 gttctaggaa gactgacagt ttgggtctgt gtcattgccc aaatctcatg ttaaattgta 5220
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FIGURE 16E

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FIGURE 16F

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FIGURE 16G

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FIGURE 16H

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ggaggccccc cagccccaaa ctgcaccacc tggccgtgga caccggt

12047

FIGURE 17

cgagcggccc ctcagcttcg gcgcccagcc ccgcaaggct cccggtgacc actagagggc 60
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catttcacca ccaccatg 858

FIGURE 18

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tgcaagacac tgcccatgcc aatcatcctg aaaagcagct ataaaaagca ggaagctact 420
ctgcaccttg tcagtgaggt ccagatacct acag 454

g atg acc ggc tca acc atc gcg ccc aca acg gac tat cgc aac acc act	49
Met Thr Gly Ser Thr Ile Ala Pro Thr Thr Asp Tyr Arg Asn Thr Thr	
1 5 10 15	
gct acc gga cta aca tct gcc cta aat tta ccc caa gtt cat gcc ttt	97
Ala Thr Gly Leu Thr Ser Ala Leu Asn Leu Pro Gln Val His Ala Phe	
20 25 30	
gtc aat gac tgg gcg agc ttg gac atg tgg tgg ttt tcc ata gcg ctt	145
Val Asn Asp Trp Ala Ser Leu Asp Met Trp Trp Phe Ser Ile Ala Leu	
35 40 45	
atg ttt gtt tgc ctt att att atg tgg ctt att tgt tgc cta aag cgc	193
Met Phe Val Cys Leu Ile Ile Met Trp Leu Ile Cys Cys Leu Lys Arg	
50 55 60	
aga cgc gcc aga ccc ccc atc tat agg cct atc att gtg ctc aac cca	241
Arg Arg Ala Arg Pro Pro Ile Tyr Arg Pro Ile Ile Val Leu Asn Pro	
65 70 75 80	
cac aat gaa aaa att cat aga ttg gac ggt ctg aaa cca tgt tct ctt	289
His Asn Glu Lys Ile His Arg Leu Asp Gly Leu Lys Pro Cys Ser Leu	
85 90 95	
ctt tta cag tat gat taa	
Leu Leu Gln Tyr Asp	307
100	

FIGURE 19